

FINAL EXAM ANSWER KEY
BICD100 GENETICS
FALL 2005
PROF. REINAGEL
class statistics at end

QUESTION 1	TOTAL POINTS:	6.5	PARTS:	a – g
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1. In an experiment like Mendel's, true-breeding plants with flat flower petals were crossed with true-breeding plants with ruffled flower petals. The F1 generation plants had ruffled flower petals. You allow F1 plants to self-pollinate to form a second generation, and analyzed the seeds of the resulting F2 generation.

a. Assign your symbols (½ pt)

Dominant allele: A phenotype: ruffled

Recessive allele: a phenotype: flat

b. What is the genotype of the F1 plant? Aa (½ pt)

c. What types of **gametes** does the F1 plant produce, in what ratio?
1 A : 1 a (½ pt)

d. What are the **genotypes** of the F2 generation plants, in what ratio?
1 AA : 2 Aa : 1 aa (½ pt)

e. What are the **phenotypes** of the F2 generation plants, in what ratio?
3 ruffled : 1 flat (½ pt)

f. Two genotypes of F2 plants have the same phenotype. To which of the pure breeding parental plants should you cross them to tell them apart? What ratio of phenotypes do you expect in the resulting progeny in each case?

Genotype of the parent to which you will cross: aa (½ pt)

For F2 plants with genotype Aa
 expect progeny phenotypes in ratio 1 ruffled : 1 flat (½ pt)

For F2 plants with genotype AA
 expect progeny phenotypes in ratio 1 ruffled : 0 flat (½ pt)

g. In your actual experiment you obtained 184 ruffled + 40 flat-petaled F2 plants. Use a Chi Square test to determine whether the observed data ARE CONSISTENT WITH Mendel's predicted ratio, with a confidence threshold of 0.05. Show your work and put a box around the χ^2 value, the P value, and your yes/no answer below. (2 ½ pts)

O	E	(O-E) ²	(O-E) ² /E
184	168	256	1.524
40	56	256	4.571

Chi square (χ^2) = 6.095

Df= 2-1=1 0.05>P>0.025

Circle one:

YES the data are consistent with the predicted ratio

NO the data are significantly different from the predicted ratio

Partial credit on chi square test:
 ½ pt for correct obs and exp values
 ½ pt for correct chi square value
 ½ pt for correct df
 ½ pt for correct p value
 ½ pt for circling "no"

Table 2-2 Critical Values of the χ^2 Distribution

df	P									df
	0.995	0.975	0.9	0.5	0.1	0.05	0.025	0.01	0.005	
1	.000	.000	0.016	0.455	2.706	3.841	5.024	6.635	7.879	1
2	0.010	0.051	0.211	1.386	4.605	5.991	7.378	9.210	10.597	2
3	0.072	0.216	0.584	2.366	6.251	7.815	9.348	11.345	12.838	3
4	0.207	0.484	1.064	3.357	7.779	9.488	11.143	13.277	14.860	4
5	0.412	0.831	1.610	4.351	9.236	11.070	12.832	15.086	16.750	5
6	0.676	1.237	2.204	5.348	10.645	12.592	14.449	16.812	18.548	6
7	0.989	1.690	2.833	6.346	12.017	14.067	16.013	18.475	20.278	7
8	1.344	2.180	3.490	7.344	13.362	15.507	17.535	20.090	21.955	8
9	1.735	2.700	4.168	8.343	14.684	16.919	19.023	21.666	23.589	9
10	2.156	3.247	4.865	9.342	15.987	18.307	20.483	23.209	25.188	10
11	2.603	3.816	5.578	10.341	17.275	19.675	21.920	24.725	26.757	11
12	3.074	4.404	6.304	11.340	18.549	21.026	23.337	26.217	28.300	12
13	3.565	5.009	7.042	12.340	19.812	22.362	24.736	27.688	29.819	13
14	4.075	5.629	7.790	13.339	21.064	23.685	26.119	29.141	31.319	14
15	4.601	6.262	8.547	14.339	22.307	24.996	27.488	30.578	32.801	15

QUESTION 2	TOTAL POINTS:	6.0	PARTS:	a – c
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2. Wild-type fruit flies have brown bodies and red eyes. You have a pure-breeding yellow-bodied strain of flies (otherwise normal), and another pure-breeding strain of flies with peach-colored eyes (otherwise normal). The allele for yellow-body is recessive to the allele for brown-body, and the allele for peach-eyes is recessive to the allele for red-eyes. You cross males from the yellow-bodied strain to females from the peach-eyed strain to obtain an F1 generation.

- a. You cross the F1 flies to one another and analyze the F2 progeny. If everything is working the way Mendel predicted for a simple dihybrid cross with independently segregating traits, what phenotypic classes do you expect to find, and in what ratios? (Simply list the possible phenotypes and state the relative frequencies).

9 Brown Red: 3 Brown peach : 3 yellow Red : 1 yellow peach 1 pt

- b. The yellow-body trait turns out to be caused by a recessive allele of a gene located on the X chromosome of flies. Using this additional information, state the genotype and phenotype of male and female flies in the parental and F1 generations for both eye color and body color.

	Genotype	phenotype	
Female parent	<u> $X^B X^B r r$ </u>	<u> brown body, peach eyes </u>	½ pt
Male parent	<u> $X^b Y R R$ </u>	<u> yellow body, red eyes </u>	½ pt
Female F1	<u> $X^B X^b R r$ </u>	<u> brown body, red eyes </u>	½ pt
Male F1	<u> $X^B Y R r$ </u>	<u> brown body, red eyes </u>	½ pt

- c. Even though body-color is sex linked, you hypothesize that the body-color and eye-color traits still assort independently from one another, just as Mendel would have expected. Predict the phenotypic ratios in the F2 generation in this case. Give the phenotypic ratios for males, for females, and overall. Use Punnet square(s), tree diagram(s), or probability equation(s) to justify your conclusions. You must SHOW YOUR WORK for full credit.

Example of satisfactory work shown:

	$X^B R$	$X^B r$	$Y R$	$Y r$
$X^B R$	Brown red female	Brown red female	Brown red male	Brown red male
$X^B r$	Brown red female	Brown peach female	Brown red male	Brown peach male
$X^b R$	Brown red female	Brown red female	yellow red male	yellow red male
$X^b r$	Brown red female	Brown peach female	yellow red male	yellow peach male

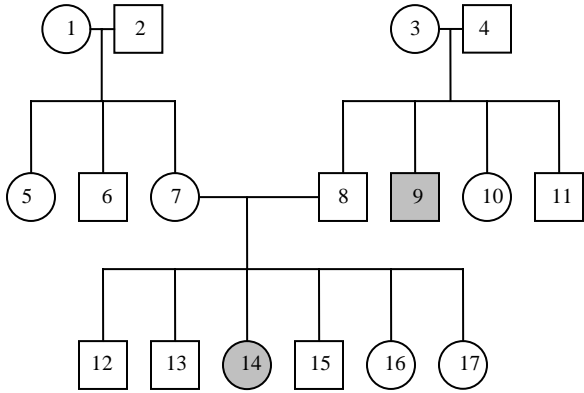
Phenotypic ratios among FEMALE F2: 1 pt
 6 Brown Red: 2 Brown peach : 0 yellow Red : 0 yellow peach
 (3 Brown Red: 1 Brown peach is also a correct answer)

Phenotypic ratios among MALE F2: 1 pt
 3 Brown Red: 1 Brown peach : 3 yellow Red : 1 yellow peach

Phenotypic ratios in F2 overall: 1 pt
 9 Brown Red: 3 Brown peach : 3 yellow Red : 1 yellow peach

QUESTION 3	TOTAL POINTS:	3.0	PARTS:	a, b
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3. An individual came into a genetic clinic because of a harmless but very rare trait of having pointy ears. She reported that she had an uncle with pointy ears too, but no other family history of the trait. She reported her family tree as follows:



a. Assuming the trait is hereditary, state the most likely mode of inheritance, and provide the MOST convincing reason for EACH conclusion you reached about the mode of inheritance.

Mode of inheritance autosomal recessive 1 pt

Reason 1 recessive because affected individuals can have both parents not affected ½ pt

Reason 2 autosomal, because if it were X-linked, individual 8 would have to be affected ½ pt

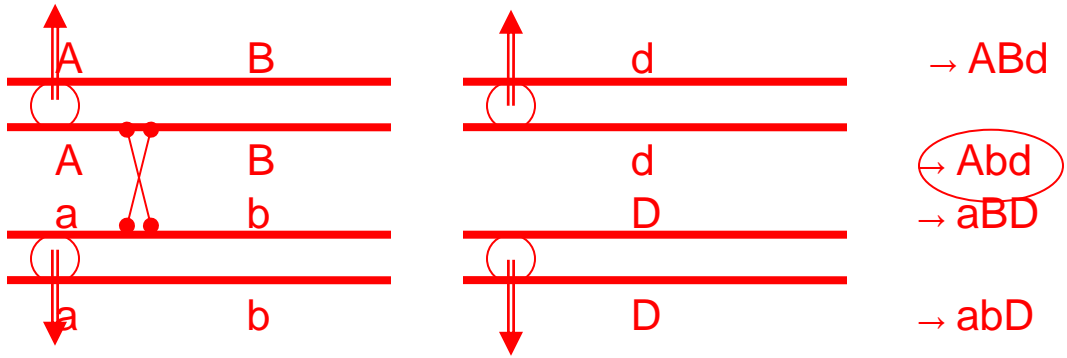
(must give one reason for autosomal and one reason for recessive)

b. All individuals are identified by numbers in the pedigree above. List the individuals that MUST be heterozygous for the trait.

 3,4, 7,8 1 pt

QUESTION 4	TOTAL POINTS:	2.5	PARTS:	(one part)
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4. You cross a mouse with genotype AABbCC to a mouse with genotype aabbdd to make an F1 mouse: AaBbDd. You know that the A gene is tightly linked to the centromere of chromosome 1, the B gene is somewhere on chromosome 1, and the D gene is on chromosome 4. You cross your F1 mouse with a mouse from the aabbdd parental strain. One of the resulting F2 progeny has the phenotype A_bbdd. Diagram the first and second divisions of a specific meiosis in the F1 mouse that could have produced the necessary gamete to explain the F2 mouse's phenotype. Your diagram should clearly indicate the direction of segregation of the homologs and sister chromatids, any necessary crossover events, and the genotypes of all four meiotic products. Circle the gamete that explains the phenotype of the F2 mouse in question.



QUESTION 5	TOTAL POINTS:	3.5	PARTS:	a – d
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5. Unicorns have typical diploid eukaryotic genetics. Normal unicorns are wild, with blue eyes and pure white coats. You are studying three genes in unicorns whose recessive mutant alleles cause the phenotypes of tameness (tame), mottled coats (mottled), and purple eyes (purple). You cross unicorns from a pure-breeding purple strain to unicorns from a pure breeding tame mottled strain to obtain F1 unicorns. **SHOW YOUR WORK.**

a. State the phenotype and genotype of the F1: **½ pt**

Parents: mottled tame X purple

F1 mt+

++p

You cross these F1 unicorns to a pure-breeding mottled, purple, tame strain and analyze 500 F2 progeny. You obtain the following data:

111	mottled purple tame	mpt
13	purple tame	+pt
14	tame	++t
119	mottled tame	m+t
11	mottled purple	mp+
114	wild type	+++
106	purple	+p+
12	mottled	m++

b. Determine the recombination frequency (map distance) between the mottled and tame genes: **1 pt**

Parental = mt or ++

Nonparental = m+ or +t = 13 + 14 + 11 + 12 = 50

$$\text{r.f.} = \frac{\# \text{ nonparental}}{\text{total}} \times 100 = \frac{50}{500} \times 100 = 10 \text{ cM}$$

c. Determine the recombination frequency (map distance) between the mottled and purple genes: **1 pt**

Parental = m+ or +p = 119 + 106 + 12 + 13 = 250

Nonparental = ++ or mp = 111 + 114 + 14 + 11 = 250

$$\text{r.f.} = \frac{\# \text{ nonparental}}{\text{total}} \times 100 = \frac{250}{500} \times 100 = 50 \text{ cM (unlinked)}$$

d. Determine the recombination frequency (map distance) between the purple and tame genes: **1 pt**

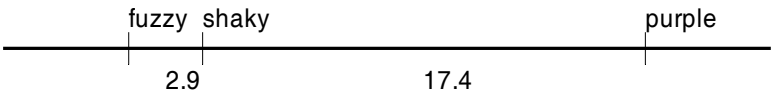
Parental = +t or p+

Nonparental = ++ or pt = 111 + 13 + 114 + 12 = 250

$$\text{r.f.} = \frac{\# \text{ nonparental}}{\text{total}} \times 100 = \frac{250}{500} \times 100 = 50 \text{ cM (unlinked)}$$

QUESTION 6	TOTAL POINTS:	4.5	PARTS:	a – b
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6. You are interested in three genes in bacteriophage. The recessive mutant alleles cause plaque phenotypes that were creatively named fuzzy, shaky, and purple. Another lab published the following map of the three genes:



To verify the published map, you cross a purple shaky phage strain with a fuzzy phage strain by co-infecting *E. coli* at a high multiplicity of infection (every bacterium infected with both types of phage). You plate the resulting lysate and analyze the phenotypes of the plaques caused by the progeny phage.

a. State the genotypes of the two parent phage strains:

+ s p and f + + 1/2 pt

b. List all eight of the possible phenotypes that could result from this cross. If 400 phage plaques were examined from this cross, how many plaques of each of the eight phenotypic classes would you expect? 4 pt

Expected double xo = $0.029 * 0.174 * 400 = 2$ --> 1 ++p, 1 fs+
 f – s singles = $(0.029 * 400) - \text{doubles} = 11.6 - 2 = 9.6$ --> 5 +++ , 5 fsp
 s – p singles = $(0.174 * 400) - \text{doubles} = 69.6 - 2 = 67.6$ --> 34 +s+ , 34 f+p
 parentals = total – singles – doubles =
 $400 - 10 - 68 - 2 = 320$ --> 160 +sp, 160 f++

- Progeny classes:
- 1 purple
 - 1 fuzzy shaky
 - 5 wild type
 - 5 fuzzy purple shaky
 - 34 shaky
 - 34 fuzzy purple
 - 160 fuzzy
 - 160 purple shaky

TOTAL 400

Partial credit:
 +0.5 for every correct number that is supported by correct work shown

QUESTION 7	TOTAL POINTS:	6	PARTS:	a –c
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7. You are studying a type of yeast that can grow either as a haploid or a diploid. Sporulation of the diploids produces unordered tetrads.

- a. You cross a MAT a xyl1- haploid to a MAT α XYL1+ haploid and then sporulate the resulting diploids. You analyze 100 tetrads, with the following results:

Type I	II	III
MAT α xyl1-	MAT a xyl1-	MAT a xyl1-
MAT α xyl1-	MAT a xyl1-	MAT α xyl1-
MAT a XYL1+	MAT α XYL1+	MAT a XYL1+
MAT a XYL1+	MAT α XYL1+	MAT α XYL1+
17	16	67

What can you conclude about the linkage of the two genes to one another and to their centromere(s)?

$$PD=16, NPD=17, TT = 67$$

PD=NPD so unlinked

TT = 2/3 so both unlinked to centromeres

2 points

- b. You cross a PHO2+ BIB1+ haploid to a pho2- bib1- haploid to obtain a diploid. You sporulate the diploid and analyze 100 tetrads, with the following results:

Type I	II	III
PHO2+ bib1-	pho2- bib1-	pho2- bib1-
PHO2+ bib1-	PHO2+ bib1-	pho2- bib1-
pho2- BIB1+	pho2- BIB1+	PHO2+ BIB1+
pho2- BIB1+	PHO2+ BIB1+	PHO2+ BIB1+
1	37	62
npd	tt	pd

What can you conclude about the linkage of the two genes to one another and to their centromere(s)?

2 points

$$PD=62, NPD=1, TT = 3$$

PD>>NPD so linked

NPD exist so there are DCOs;

$$d = \frac{\frac{1}{2} TT + 3NPD}{TOTAL} = \frac{\frac{1}{2} 37 + 3}{100} = 21.5cM$$

Can't tell anything about centromeres because on same chromosome

- c. When determining the distance between two linked genes on the basis of unordered tetrad data, there are two different equations you can use depending on whether or not double crossovers were observed. Call the difference between the two equations the “correction term” for double crossovers. What is the correction term and where does it come from? In other words, how exactly are double crossovers taken into account in this equation?

2 points

The correction term is + 3NPD

Where it comes from:

There are 4 kinds of DCO's depending on strands involved, one of which gives PD, 2 give TT, one gives NPD. Therefore #DCO's = 4NPD

And the number of TT's that are DCO's (not SCO's) = 2NPD

THUS

Recombinant spores due to single crossovers = $\frac{1}{2}$ (TT - 2NPD)

Recombinant spores due to double crossovers = 4NPD

(the $\frac{1}{2}$ term for half the spores being recombinant is cancelled out by a x2 term for having two crossovers)

$$\text{Distance} = \frac{\frac{1}{2}(\text{TT} - 2\text{NPD}) + 4\text{NPD}}{\text{TOTAL tetrads}} \times 100$$

$$= \frac{\frac{1}{2} \text{TT} + 3\text{NPD}}{\text{TOTAL}} \times 100$$

QUESTION 8	TOTAL POINTS:	5	PARTS:	a –c
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8. You have a wild-type strain of E. coli with the genotype

A B C D E F

You introduce an F+ plasmid into your wild-type strain and isolated a few Hfr derivative strains that you call Hfr1, Hfr2, and Hfr3.

You are studying several new genes in E. coli with interesting phenotypes. You obtain a multiply mutant strain with chromosomal genotype:

a b c d e f

a) You mate each Hfr strain to your multiply-mutant strain in a separate experiment. At various times you interrupt the matings and plate the bacteria under conditions in which only the recipient strain can grow. You obtain the following earliest-time-of-entry data, in minutes:

Gene	Hfr1	Hfr2	Hfr3
A	-	26	16
B	-	-	5
C	11	11	31
D	13	9	-
E	7	15	27
F	-	31	11

Draw a map of these genes that is consistent with the data, including all the genes and Hfr origins, the distances between them (in minutes), and the direction of transfer of each Hfr. **(3 pts)**

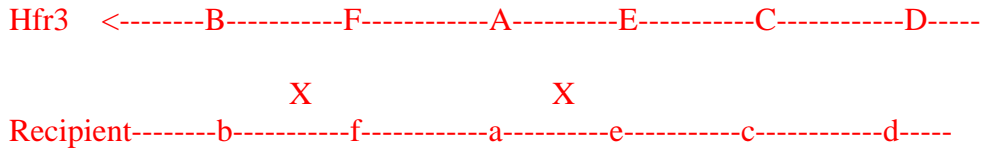
Direction of Hfr origins: 1 pt
 Order of genes: 1 pt
 Distances between genes: 1 pt

Hfr3 5 B 6 F 5 A 4 Hfr1 7 E 4 C 2 D 9 Hfr2
 <-----<----->

If you showed a circular map, must either to show the distance btwn Hfr2 and Hfr3 as unknown, or acceptable to compute it by assuming 100' total map size.

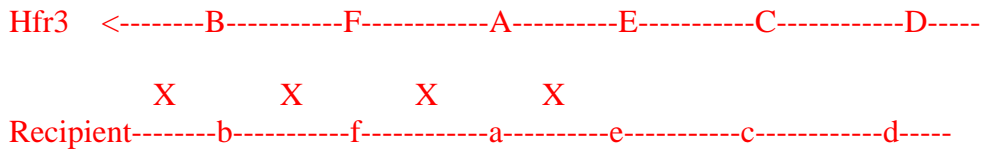
b) Among the progeny from the Hfr3 mating above, you find one that has the genotype:
A b c d e F

Draw out the gene transfer and crossover(s) that produced this outcome: (1 pt)



c) Among the progeny from the Hfr3 mating above, you find one that has the genotype:
A B c d e f

Draw out the gene transfer and crossover(s) that produced this outcome: (1 pt)



QUESTION 9	TOTAL POINTS:	5	PARTS:	a –c
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9. A recessive mutation in rats causes a defect in courtship behavior. The affected individuals are perfectly viable, but never reproduce. (The wild type dominant allele is A, the recessive disease allele is a). In a large population study you determine that 1 in 8,000 rats is affected with this disease. This result is stable over several generations. Assume that the population is very large, there are no migrations, and that mating is random.

- a. What are the frequencies of the dominant and recessive alleles in the gametes of this population?

(2pt)

$$q^2 = 1/8000$$

$$q = \sqrt{1/8000} = 0.0112 \quad = \text{frequency of recessive gamete "a"}$$

$$p = 1 - q = 0.9888 \quad = \text{frequency of dominant gamete "A"}$$

- b. What are the frequencies of the AA, Aa, and aa genotypes in the adult population?

(2pt)

$$\text{Freq}(AA) = p^2 = 0.989^2 = 0.9778$$

$$\text{Freq}(Aa) = 2pq = 2 \times 0.011 \times 0.989 = 0.0221$$

$$\text{Freq}(aa) = q^2 = 1/8000 = 1.25 \times 10^{-4}$$

- c. What is the mutation rate at which A alleles mutate into a alleles?

(1pt)

$$\text{mutation rate} = q^2 = 1/8000 = 1.25 \times 10^{-4}$$

d. You take the diploids from each of the crosses shown in (c) and sporulate them. The possible types of tetrads you could get are:

- I 4 cof+ : 0 cof-
- II 3 cof+ : 1 cof-
- III 2 cof+ : 2 cof-
- IV 1 cof+ : 3 cof-
- V 0 cof+ : 4 cof-

Assuming there are no unusual interactions between the genes, which type(s) of tetrads do you expect to get from the diploids that have cof- phenotypes? Explain your answer.

Non complement so same gene; expect all PD, type V **1 pt**

Assuming there are no unusual interactions between the genes, which type(s) of tetrads do you expect to get from the diploids that have cof+ phenotypes? Explain your answer.

Complement so different genes; can get PD (type V), **1 pt**
 NPD (type III), and/or TT (type IV).

e. Using these and other mutants, you eventually identify many genes that are necessary for growth on coffee, including the genes COF1, COF2, and COF3. You conduct a cross-feeding experiment with the following results:

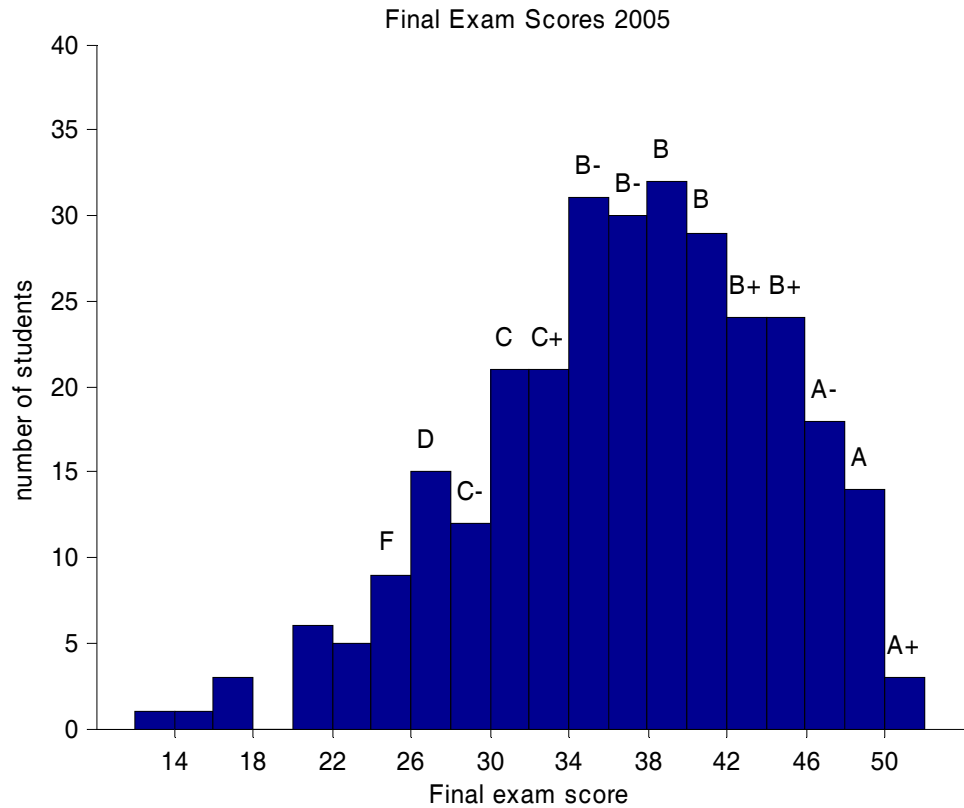
- cof1- mutants incubated in coffee medium won't grow, but accumulate something that cof2- mutants can grow on
- cof3- mutants incubated in coffee medium won't grow, but accumulate something that either cof1- or cof2- mutants can grow on

Suggest a pathway for conversion of a precursor in coffee to an essential nutrient, showing the point of action of the products of the three COF genes consistent with the cross-feeding data:

cof2 cof1 cof3
 precursor ----> x -----> y -----> nutrient

2 pts

This class is not curved. Statistics are provided for your information only.



Extra credit rule for final exam:

If your guess was off by	you got this much extra credit
0-1	2
1.5-2	1.5
2.5-3	1
3.5-4	0.5

In the course overall: the mean score was 78/100, with an almost-normal distribution peaking around 80 (solid B). In all, 49 students (16% of class) earned an A- or higher grade, and 5 exceptional students earned perfect scores in the course (A+).